--Figure 75 shows isotope clusters observed in the m/z range where RNA-ligand complexes are expected are further analyzed by peak centroiding and integration. Figure 76 depicts data tabulated and stored in a relational database. Peaks which correspond to complexes between the RNA target and ligands are assigned and recorded in the database. If an internal affinity standard is employed, a relative Kd is automatically calculated from the relative abundance of the standard complex and the unknown complex and recorded in the database. Figure 77 depicts a flow chart for one computer program for effectuating certain aspects of the present invention.--

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In the Claims:

Please cancel claims 1-86, 101-107 and 109 without prejudice to their presentation in another application, and amend claims 87, 88, 94, 95 and 108 to read as follows.

87. (Amended) A purified and isolated RNA comprising a joined sequence of at least twenty-nine but not more than seventy nucleotides and having secondary structure defined by:

five nucleotides forming a first side of a first double stranded region;

four nucleotides forming a first side of a first end loop region;

five nucleotides forming a second side of said first double stranded region;

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two nucleotides forming a bulge between said first double stranded region and a second double stranded region;

five nucleotides forming a first side of said second double stranded region;

three nucleotides forming a second end loop region; and

five nucleotides forming a second side of said second double stranded region.

88. (Amended) The RNA of claim 87 wherein said nucleotides forming said first side of said first double stranded region are of the sequence NNNGA, UAAGA, AAAGA, UAUGA, or UUUGA and said nucleotides forming said second side of said first doubled stranded region are of the sequence UUNNG, UUUUG, or UUCUG.

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94. (Amended) A purified and isolated RNA comprising a joined sequence of nucleotides having